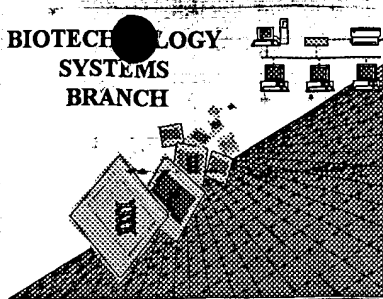


Goldberg

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED

DEC 09 2000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/580,797

Source: 1655

Date Processed by STIC: 11/22/2000

RECEIVED

DEC 11 2000

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/580,797

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

J. Goldberg

1655

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/580,797

DATE: 11/22/2000
TIME: 11:23:21

Input Set : A:\IWEN Sequence Listing ('797).txt
Output Set: N:\CRF3\11222000\I580797.raw

3 <110> APPLICANT: Iwen, Peter C.
4 Hinrichs, Steven H.
5 Henry, Travis
6 Board of Regents of the University of Nebraska
8 <120> TITLE OF INVENTION: Materials and Methods for Molecular
9 Detection of Clinically Relevant Pathogenic Fungal Species
11 <130> FILE REFERENCE: UNMC 63149
13 <140> CURRENT APPLICATION NUMBER: 09/580,797
14 <141> CURRENT FILING DATE: 2000-05-30
16 <160> NUMBER OF SEQ ID NOS: 39
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

697 <210> SEQ ID NO: 37
698 <211> LENGTH: 565 *599 shown*
699 <212> TYPE: DNA
700 <213> ORGANISM: Aspergillus niger
702 <400> SEQUENCE: 37
703 tccqlaagtg aacctgcgga agqatcatta ccgaqtgcgg gtcctttggg cccaacctcc 60
704 caccggtgtc tattgtaccc tgttgcctcg gcgggccgcg cgtttgtcgg ccgcgggggg 120
705 ggcgcctctg ccccccgggc cgtgcgcgcg cggagacccc aacargaaac ctgtctgaaa 180
706 gcgtgcacgc tgaqltgatt gaatgcacac aqltaaaact ttcaacaatg gatctcttgg 240
707 ttccqgcacg gatgaagaac qcagcgaaat gcgataacta atgtgaaltg cagaattcag 300
708 tgaatcatcg agtctttgaa cgcacattgc gccccctggt attccggggg gcatgcctgt 360
709 ccgagcgtca ttgctgcctt caagcccggc ttgtgtgttg ggtgcgcgtc cccctctcgg 420
710 gggggacggg ccggaaggc agcggcgga ccgcgtccga tctcggagcg tatggggcct 480
711 tgtcacatgc tctgtaggat tggccggcgc ctgccgacgt ttccaacca ttctttccag 540
E--> 712 gttgacctcg gatcaggtag ggataccgcg tgaacttaag catatcaata agcggagga 599

see next page for more errors

09/580,197 2

RECEIVED

DEC 09 2000

<210> 10
 <211> 563
 <212> DNA
 <213> Fusarium solani

TECH CENTER 1600/2900

RECEIVED

<400> 10
 ggaagtaaaa gtcgtaacaa ggtttctgta ggtgaacctg cagaaggatc attcgagtta
 tacaactcat caaccctgtg aacataccta taacgttgcc tcggcgggaa cagacggccc
 cgtaacacgg gccgcccccg ccagaggacc ccctaactct gtttctataa tgtttcttct
 gagtaaacaa gcaaataaat taaaactttc aacaacggat ctcttggtc tggcacgat
 gaagaacgca gcgaaatgag ataagtaatg tgaattgcag aattcagtga atcatcgaat
 ctttgaacgc acattgcgcc cgccagtatt ctggcgggca tgcctgttcg agcgtcatta
 caaccctcag ggccccgggc ctggcggttg ggatcgggcg aagccccctg cgggcacacac
 gccgtcccc aaatacagtg gcggggcccg ccgcaaactt ccattgcggt anataacta
 acacctcgca aatggagaga gggggcgcc acgccgtaaa acaccaact tctgaatggt
 gacctcgaat caagtaggaa tac

60
 120
 180
 240
 300
 360
 420
 480
 540
 563

DEC 11 2000

TECH CENTER 1600/2900

7 see
 item 10
 on Enon

*This error appears in subsequent
 sequences, too.*

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

*Summary
 sheet*

VERIFICATION SUMMARY

DATE: 11/22/2000

PATENT APPLICATION: US/09/580,797

TIME: 11:23:22

Input Set : A:\IWEN Sequence Listing ('797).txt

Output Set: N:\CRF3\11222000\I580797.raw

L:198 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
 L:198 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
 L:198 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
 L:198 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
 L:198 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
 L:328 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
 L:328 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
 L:328 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
 L:328 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
 L:328 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
 L:479 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
 L:479 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
 L:479 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
 L:479 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
 L:479 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
 L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
 L:517 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
 L:517 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
 L:517 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
 L:517 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
 L:518 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
 L:518 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
 L:518 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
 L:518 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
 M:340 Repeated in SeqNo=27
 L:552 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
 L:552 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
 L:552 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
 L:552 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
 L:552 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
 L:558 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
 L:558 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
 L:558 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
 L:558 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
 M:340 Repeated in SeqNo=29
 L:610 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
 L:610 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:610 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
 L:610 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
 L:610 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
 L:611 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
 L:611 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:611 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
 L:611 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
 M:340 Repeated in SeqNo=32
 L:612 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
 L:612 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:612 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32

VERIFICATION SUMMARY DATE: 11/22/2000
PATENT APPLICATION: US/09/580,797 TIME: 11:23:22

Input Set : A:\IWEN Sequence Listing ('797').txt
Output Set: N:\CRF3\11222000\I580797.raw

L:612 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
L:613 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:613 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
L:614 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:614 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:614 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:614 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
L:615 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:615 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:630 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
M:340 Repeated in SeqNo:33
L:712 M:252 E: No. of Seq. differs, <211>LENGTH:Input:565 Found:599 SEQ:37